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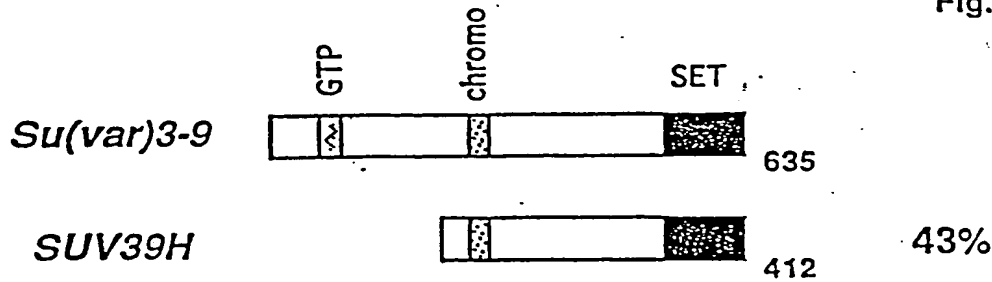
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 E(z) —1MNSTKVPPPEWKRRVKSEYIKIRQQKRYKRADEIKEAWIRNWDEN 45
 51 ERTEILNQEWKQRRIQPVHILTSVSSILRGTRCSVTSDDLDFP..TQVIPL 98
 46 RNVQDLYCESKVVQAKPYD....PPHVDCVKRAEVTSYNGIPSGPQKVP 91
 99 KTLNAVASVPIMYSWSPLQONFMVEDETVLHNIPYMGDEVLDQDGTFFIEE 148
 92 CVINAVTPIPTMYTWAPTQONFMVEDETVLHNIPYMGDEVLDKDGKFFIEE 141
 149 LIKNYDGVHGDRECGFINDEIFVELVNAL..... 178
 142 LIKNYDGVHGDKDP SFMDDAIFVELVHALMRSYSKELEEAAPSTSTAIK 191
 179GOYNDDDDDDDDGDDPE.....EREKQKDLED.....H 206
 192 TEPLAKSKQGEDDGVVDVADCESPMKLEKTESKGDLDVEKKETEETVE 241
 207 RDDKESRPPRK.....FPSDKIFEAISSMFPDKGTAEELKEKYKELTE 249
 242 TEDADVKEPAVEEVKDKLPFPAPIIFQAISANFPDKGTAEELKEKYIELTE 291
 250 QQLPGALPPE@P@NIDGPNKSVQREQSLHSFHTLE@P@FKYD@LHPP 299
 292 HQDPER.POB@P@NIDGIKAESVSRERTMHSFHTLE@P@FKYD@LHRL 340
 300 ..HATPNTYKRNKTETALDNKE@G@P@Q@HLEGAKFAAALTAERIKTPP 347
 341 QGHAGPNLQKRRYPELKPFAB@NS@MLIDGMKEKLA...DSKTTP 386
 348 KRPGGRRRGRLPNNSSRPSTPTINVLESKDTSDREAGTETGGENNDKEE 397
 387IDSCNEASSEDSDNSNSQFSNKDFNH 412
 398 EEKDET.SSSSEANSRCOTPIKMKPNIEPPENVEWSGAEASMFVRLIGT 446
 413 ENSKDNGLTVNSAAVAEINSIMAGMNTSTQCV.WTGADQALYRVLHKV 461
 447 YYDNE@AIARLIGTK@RQVYEFVRKESSIIAPAPAEDVDTPPRKKKKKH 496
 462 YLKNY@AIARNMLTK@RQVYEFQKEDAEFSFEDLQDFTPPRKKKKKQ 511
 497 RLWAAH@PKIQLKKDGSSNHVYNYQ@DHPROP@SS@P@IAONE@EK 546
 512 RLWSLH@PKIQLKKDGSSNHVYNYTH@DHPGHE@OM@P@Q@TQNS@EK 561
 547 @SSSE@QNRFP@P@K@Q@NTK@P@LAVRE@PDI@Q@G@ADQHWDS 596
 562 @SSSD@QNRFP@P@K@Q@NTK@P@LAVRE@PDI@Q@G@ADQFKL 610
 597 KNVSE@KNC SIQRGSKHLLIAPSDVAGNGIE@RDPVOKNEP@SEYCGE@ 646
 611 TKIT@QVVCVQGLHKHLLMAPSDIAGNGIE@RDPVOKNEP@SEYCGE@ 660
 647 SODEADRRGKVYDKYMCSELENENDEWVDAIRKNGKREANHSVNPCK 696
 661 SODEADRRGKVYDKYMCSELENENDEWVDAIRKNGKREANHSVNPCK 710
 697 RYVMAVNGH@RIGIEAKRAI@QGELE@P@D@Y@SOADAL@Q@GEREMETP 746
 711 RYVMAVNGH@RIGIEAKRAI@QGELE@P@D@Y@SOADAL@Q@GEREMETP 760

Fig. 1

C-rich
75%

SET
88%

Fig. 2



Su(var)3-9
SUV39H

```

1 MAENLKGCSSVCKSSWNQLQDLCLRLAKLSCPALGISKRNLVDEEVLQGLD 50
      :: ||| ....
207 .....MGVIAKRPPKGG.....EYVVERIEG 226
51 YKKIRLQENAGIVKRGYHSESTEDPHNLK..... 81
      :: ||| ....
227 VENDDGCEVTRKGGHSESEVTEHIANVADCAEMKFFVERHQQLYETY 276
82 CVRIKQFHKDLERELLRRHRSKTPRHLDPLSLANYLVQKAKORRALRR 130
      :: ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: |||
277 IAKITTELEKQLEALPIMENITVAEVDAYEPLNLQIDLILLAQYRAAGSR 326
131 WEQE.....LNAKRSHLGR.....IT 146
      :: ||| :: ||| :: |||
327 SQREPQKIGERALKSMQIKRAQFVRRKQLADLALFEKRMNHVEKPSPPIR 376
147 VENEVDLDGPPRAFVYINEYRVGEGITLNQVA.VG...DCLWAPTGG 195
      ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: |||
377 VENNIDLDTIDSNFMYIHDNIIGKDVPKPEAGIV...EDTEECTASTK 426
196 PGASL..HKFAYNDQG.QVRIRAGLPIYNSH...PNNRVVQKGR 242
      :: ||| :: ||| :: ||| :: ||| :: ||| :: |||
427 GARFAGELFAYERSTRRLRLRPGSAIYNSH...SSSNRLVQHGRQ 476
243 YDLCIFRTHGRGWGVRTLEKIRKNSFVMEVLEHETSEELERREOFLYR 292
      :: ||| :: ||| :: ||| :: ||| :: ||| :: |||
477 VPLVLFKTANGSGGCVRAATALRGDEVCEYTELTSDEANERGRAYD 526
293 QGATYLELDLY...VEDVYVDAAYIGNESHFVNHSQDENLOVINVELDN 339
      :: ||| :: ||| :: ||| :: ||| :: ||| :: |||
527 NGRTYLELDLYNTAODSEYTDAAANYGNISHFINHSQDENLAYEPCWIEH 576
340 LDERLERIAFFATRTIRAGEELTEDYNMQVDVDVMESTRMDSNEGLAGE 389
      :: ||| :: ||| :: ||| :: ||| :: ||| :: |||
577 LNVALPHVCEETHEIKAGEELSEDYLRADNEDVEXENLSTA 618
390 GSPKRVVRECKGEESECKKLE 412
619 ...VRVPCRGRONCKVTE 635
  
```

CHROMO
39 %

SET
51 %

ABERRANT TRANSCRIPTS

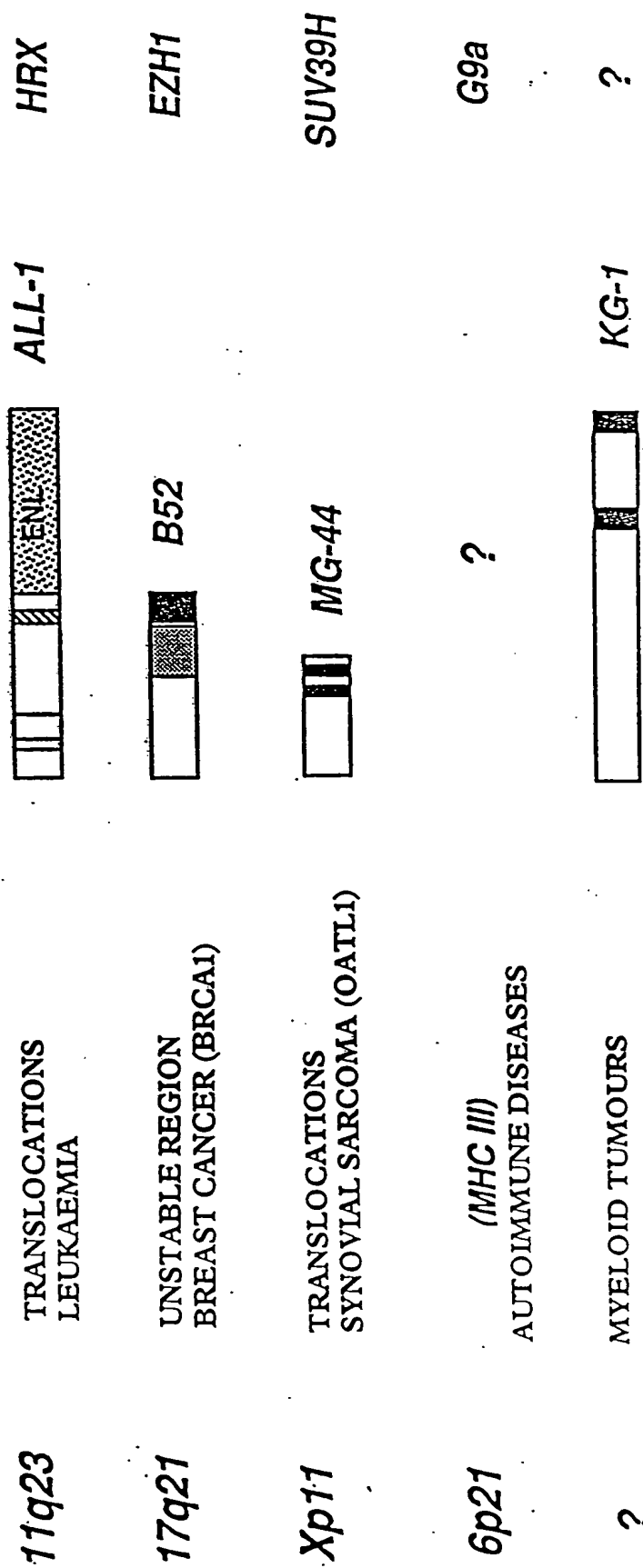



Fig. 3

Fig. 4

SET PROTEIN FAMILY

S. CEREVISIAE *YHR119*  1080

C. ELEGANS *C26E6.10*  739

DROSOPHILA M.

trx  3751

E(z)  760

Su(var)3-9  635

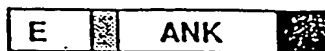
SET

HRX  3969 46%

EZH2  746 61%

SUV39H  412 43%

HUMAN

G9a  1001

HMG-1

?

Fig. 5

E(z)	SDIAGWGIFL	KEGAQKNEFI	SEYCGEITSQ	DEADRGKVY	DK..YMCSFL	50
EZH2	SDVAGWGIFI	KDPVQKNEFI	SEYCGEITSQ	DEADRGKVY	DK..YMCSFL	
HRX	SPIHGRLFC	KRNIDAGEMV	IEYAGNVIRS	IQTDKREKYY	DSKGIG.CYM	
trx	SHIHGRLYC	TKDIEAGEMV	IEYAGELIRS	TLTDKREERY	DSRGIG.CYM	
C26	SRIHGWLIA	MESIAPDEMI	VEYIGOTIRS	LVAEEREKAY	ERRGIGSSYL	
YHR	SAIHNGWLYA	LDSIAAKEMI	IEYVGERIRQ	PVAEMREKRY	LKNGIGSSYL	
Su3-9	ANGSGWGVRA	ATALRKGEFV	CEYIEEILTS	DEANERBKAY	DDNG..RTYL	
SUV39H	DDGRGWGVRT	LEKIRKNSFV	MEYVGEILTS	EEAEERGGQY	DRQG..ATYL	
G9a	TAKMGWGVRA	LQTIPOGTFI	CEYVGEILSD	AEAD...V.	.RED..DSYL	
KG-1	TQNKNGGIRC	LDDIAKGSFV	CEYAEKILTD	DFADKEGL.	.EMG..DEYF	

E(z)	ENLN.....	NDFVVDATRK	GNKIREANHS	INPNCYAKVM	MVTGDH....	100
EZH2	ENLN.....	NDFVVDATRK	GNKIREANHS	VNPNCYAKVM	MVNGDH....	
HRX	ERID.....	DSEVVDAIMH	GNRAREINHS	CEPNCYSRVI	NIDGQK....	
trx	EKID.....	DNLVVDAIMR	GNAAREINHC	CEPNCYSKVV	DILGHK....	
C26	ERID.....	LHHVIDATKR	ENFAREINHS	CEPNCYAKVL	TIEGEK....	
YHR	ERVV.....	ENTVIDATKK	GGIAREINHC	CDNCTAKII	KVGRR....	
Su3-9	EDLDYNTAQD	SEYTIIDANY	GNISHEINHS	CDPNLAVFPC	WIEHLNVALP	
SUV39H	EDLDY...VE	DVYTVDAAYY	GNISHEVNHS	CDPNLQVYNV	FIDNLDRLP	
G9a	EDLONK..DG	EVYCIDARYY	ENISREINHL	CDPNIIIPVRV	FMLHQDLRFP	
KG-1	ANLDHI..ES	VEYIIDAKLE	GNLGRGLNHS	CDPNLFVQNV	FVDTHDLRFP	

△

E(z)	RTGIEAKRAY	QPGEEIFFDY	..RYGPTEQL	K.....FVGI	EREMEIV*	150
EZH2	RTGIEAKRAY	QTGEEIFFDY	..RYSQADAL	K.....YVGI	EREMEIP*	
HRX	HEVIEAMPKQ	YRGEELTYDY	..KFPIE.DA	SNKLPCNCGA	KKCRKFLN*	
trx	HELIIPAVRRE	VOGEELTYDY	..KFPFE.D.	.EKIPSCSGS	KRCRKYLN*	
C26	REVLISRTIE	KKGEELTYDY	..KFPIE...	DDKIDCLCGA	KTCRGYLN*	
YHR	REVLIALDIT	AASEELTYDY	..KFEREKDD	EERLPCLCGA	PNCKGFLN*	
Su3-9	HEVETLIPPI	KAGEELSEFY	..IRADNEDVP	YENLSTA..	
SUV39H	RTAFFATRTI	RAGEELTFDY	NMQVDPVDME	STRMDSNEGL	AGLPGSPKKR	
G9a	RTAFFSSRDI	RTGEELGFYD	GDRFW..DIK	SKYFTCQCGS	EKCKHSAEAI	
KG-1	WVAFFASKRI	RAGTELTWDY	NYEVG..SVE	GKELLCCGA	IECR.....	

E(z)
EZH2

HRX
trx
26
YHR

Su3-9 VRVECRGRD NCRKVL*
SUV39H VRIECKCGTE SCRKYLF*
G9a ALEQSRRLARL DPHPELLPEL GSLPPVNT*
KG-1GRLL*

Fig. 6/1

EZH2 length: 2600bp (coding: 90 - 2330)

1	AGGCAGTGGAGCCCGGCGGGCGGGCGGGCGGGCGGGCGACGCGCGGGAACAACG	60
61	CGAGTCGGCGCGCGGGACGAAGAATAATCATGGGCCAGACTGGGAAGAAATCTGAGAAGG M G Q T G K K S E K G	120
121	GACCAGTTTGTTGGCGGAAGCGGTGTAAAATCAGAGTACATGCGACTGAGACAGCTCAAGA P V C W R K R V K S E Y M R L R Q L K R	180
181	GGTTCAGACGAGCTGATGAAGTAAAGAGTATGTTTAGTTCCAATCGTCAGAAAATTTTGG F R R A D E V K S M F S S N R Q K I L E	240
241	AAAGAACGGAAATCTTAAACCAAGAATGGAAACAGCGAAGGATACAGCCTGTGCACATCC R T E I L N Q E W K Q R R I Q P V H I L	300
301	TGACTTCTGTGAGCTCATTGCGCGGGACTAGGGAGTGTTCGGTGACCAGTGACTTGGATT T S V S S L R G T R E C S V T S D L D F	360
361	TTCCAACACAAGTCATCCCATTAAAGACTCTGAATGCAGTTGCTTCAGTACCCATAATGT P T Q V I P L K T L N A V A S V P I M Y	420
421	ATTCTTGGTCTCCCTACAGCAGAATTTTATGGTGAAGATGAACTGTTTTACATAACA S W S P L Q Q N F M V E D E T V L H N I	480
481	TTCCTTATATGGGAGATGAAGTTTTAGATCAGGATGGTACTTTCATTGAAGAACTAATAA P Y M G D E V L D Q D G T F I E E L I K	540
541	AAAATTATGATGGGAAAGTACACGGGGATAGAGAATGTGGGTTTATAAATGATGAAATTT N Y D G K V H G D R E C G F I N D E I F	600
601	TTGTGGAGTTGGTGAATGCCCTTGGTCAATATAATGATGATGACGATGATGATGATGGAG V E L V N A L G Q Y N D D D D D D D D G D	660
661	ACGATCCTGAAGAAAGAGAAGAAAAGCAGAAAGATCTGGAGGATCACCGAGATGATAAAG D P E E R E E K Q K D L E D H R D D K E	720
721	AAAGCCGCCACCTCGGAAATTTCTTCTGATAAAATTTTGAAGCCATTTCTCAATGT S R P P R K F P S D K I F E A I S S M F	780
781	TTCCAGATAAGGGCACAGCAGAAGAACTAAAGGAAAAATATAAAGAACTCACCGAACAGC P D K G T A E E L K E K Y K E L T E Q Q	840
841	AGCTCCCAGGCGCACTTCTCCTGAATGTACCCCCAACATAGATGGACCAAATGCTAAAT L P G A L P P E C T P N I D G P N A K S	900
901	CTGTTTCAGAGAGAGCAAAGCTTACACTCCTTTTCATACGCTTTTCTGTAGGCGATGTTTA V Q R E Q S L H S F H T L F C R R C F K	960
961	AATATGACTGCTTCCTACATCCTTTTCATGCAACACCCAACTTATAAGCGGAAGAACA Y D C F L H P F H A T P N T Y K R K N T	1020
1021	CAGAAACAGCTCTAGACAACAAACCTTGTGGACCACAGTGTTACCAGCATTTGGAGGGAG E T A L D N K P C G P Q C Y Q H L E G A	1080
1081	CAAAGGAGTTTGCTGCTGCTCTCACCGCTGAGCGGATAAAGACCCCAACAAACGTCACG K E F A A A L T A E R I K T P P K R P G	1140

Fig. 6/2

1141	GAGGCCGCGAGAAGAGGACGGCTTCCCAATAACAGTAGCAGGCCCGCAGCACCCCCACCATTA	1200
	G R R R G R L P N N S S R P S T P T I N	
1201	ATGTGCTGGAATCAAAGGATACAGACAGTGATAGGGAAGCAGGGACTGAAACGGGGGAG	1260
	V L E S K D T D S D R E A G T E T G G E	
1261	AGAACAATGATAAAGAAGAAGAAGAGAAGAAAGATGAAACTTCGAGCTCCTCTGAAGCAA	1320
	N N D K E E E E K K D E T S S S S E A N	
1321	ATTCTCGGTGTCAAACACCAATAAAGATGAAGCCAAATATTGAACCTCCTGAGAATGTGG	1380
	S R C Q T P I K M K P N I E P P E N V E	
1381	AGTGGAGTGGTGTGAAGCCTCAATGTTTAGAGTCCCTCATTGGCACTTACTATGACAATT	1440
	W S G A E A S M F R V L I G T Y Y D N F	
1441	TCTGTGCCATTGCTAGGTTAATTGGGACCAAAACATGTAGACAGGTGTATGAGTTTAGAG	1500
	C A I A R L I G T K T C R Q V Y E F R V	
1501	TCAAAGAATCTAGCATCATAGCTCCAGCTCCCGCTGAGGATGTGGATACTCCTCCAAGGA	1560
	K E S S I I A P A P A E D V D T P P R K	
1561	AAAAGAAGAGGAAACACCGGTTGTGGGCTGCACACTGCAGAAAGATACAGCTGAAAAAGG	1620
	K K R K H R L W A A H C R K I Q L K K D	
1621	ACGGCTCCTCTAACCATGTTTACAACCTATCAACCCTGTGATCATCCACGGCAGCCTTGTG	1680
	G S S N H V Y N Y Q P C D H P R Q P C D	
1681	ACAGTTTCGTGCCCTTGTGTGATAGCACAAAATTTTTGTGAAAAGTTTTGTCAATGTAGTT	1740
	S S C P C V I A Q N F C E K F C Q C S S	
1741	CAGAGTGTCAAACCGCTTTCCGGGATGCCGCTGCAAAGCACAGTGCAACACCAAGCAGT	1800
	E C Q N R F P G C R C K A Q C N T K Q C	
1801	GCCCGTGCTACCTGGCTGTCCGAGAGTGTGACCCTGACCTCTGTCTTACTTGTGGAGCCG	1860
	P C Y L A V R E C D P D L C L T C G A A	
1861	CTGACCATTTGGGACAGTAAAAATGTGTCTCTGCAAGAACTGCAGTATTCAGCGGGGCTCA	1920
	D H W D S K N V S C K N C S I Q R G S K	
1921	AAAAGCATCTATTGCTGGCACCATCTGACGTGGCAGGCTGGGGGATTTTTATCAAAGATC	1980
	K H L L L A P S D V A G W G I F I K D P	
1981	CTGTGCAGAAAAATGAATTCATCTCAGAATACTGTGGAGAGATTATTTCTCAAGATGAAG	2040
	V Q K N E F I S E Y C G E I I S Q D E A	
2041	CTGACAGAAGAGGGAAAGTGTATGATAAATACATGTGCAGCTTTCTGTTCAACTTGAACA	2100
	D R R G K V Y D K Y M C S F L F N L N N	
2101	ATGATTTTGTGGTGGATGCAACCCGCAAGGGTAACAAAATTCGTTTTGCAAATCATTGG	2160
	D F V V D A T R K G N K I R F A N H S V	
2161	TAAATCCAAACTGCTATGCAAAAGTTATGATGGTTAACGGTGATCACAGGATAGGTATTT	2220
	N P N C Y A K V M M V N G D H R I G I F	
2221	TTGCCAAGAGAGCCATCCAGACTGGCGAAGAGCTGTTTTTTGATTACAGATACAGCCAGG	2280
	A K R A I Q T G E E L F F D Y R Y S Q A	

Fig. 6/3

2281 CTGATGCCCTGAAGTATGTCGGCATCGAAAGAGAAATGGAAATCCCTTGACATCTGCTAC 2340
D A L K Y V G I E R E M E I P *
2341 CTCCTCCCCCTCCTCTGAAACAGCTGCCTTAGCTTCAGGAACCTCGAGTACTGTGGGCAA 2400
2401 TTTAGAAAAAGAACATGCAGTTTGAAATTCTGAATTTGCAAAGTACTGTAAGAATAATTT 2460
2461 ATAGTAATGAGTTTAAAAATCAACTTTTTATTGCCTTCTCACCAGCTGCAAAGTGTTTTG 2520
2521 TACCAGTGAATTTTTGCAATAATGCAGTATGGTACATTTTCAACTTTGAATAAAGAATA 2580
2581 CTTGAACTTGTCAAAAAAA 2600

Fig. 7/1

SUV39H length: 2732 bp (coding: 45 - 1284)

1	TCGCGAGGCCGGCTAGGCCCGAATGTCGTTAGCCGTGGGAAAGATGGCGGAAAATTAA	60
	M A E N L K	
61	AAGGCTGCAGCGTGTGTTGCAAGTCTTCTTGAATCAGCTGCAGGACCTGTGCCGCTGG	120
	G C S V C C K S S W N Q L Q D L C R L A	
121	CCAAGCTCTCCTGCCCTGCCCTCGGTATCTCTAAGAGGAACCTCTATGACTTTGAAGTCG	180
	K L S C P A L G I S K R N L Y D F E V E	
181	AGTACCTGTGCGATTACAAGAAGATCCGCGAACAGGAATATTACCTGGTGAAATGGCGTG	240
	Y L C D Y K K I R E Q E Y Y L V K W R G	
241	GATATCCAGACTCAGAGAGCACCTGGGAGCCACGGCAGAATCTCAAGTGTGTGCGTATCC	300
	Y P D S E S T W E P R Q N L K C V R I L	
301	TCAAGCAGTTCCACAAGGACTTAGAAAGGGAGCTGCTCCGGCGGCACCACCGGTCAAAGA	360
	K Q F H K D L E R E L L R R H H R S K T	
361	CCCCCGGCACCTGGACCCAAGCTTGGCCAACCTACCTGGTGAGAAGGCCAAGCAGAGGC	420
	P R H L D P S L A N Y L V Q K A K Q R R	
421	GGGCGCTCCGTGCTGGGAGCAGGAGCTCAATGCCAAGCGCAGCCATCTGGGACGCATCA	480
	A L R R W E Q E L N A K R S H L G R I T	
481	CTGTAGAGAATGAGGTGGACCTGGACGGCCCTCCGCGGGCCTTGTGTACATCAATGAGT	540
	V E N E V D L D G P P R A F V Y I N E Y	
541	ACCGTGTGTGGTGAGGGCATCACCTCAACCAGGTGGCTGTGGGCTGCGAGTGCCAGGACT	600
	R V G E G I T L N Q V A V G C E C Q D C	
601	GTCTGTGGGCACCCACTGGAGGCTGCTGCCCCGGGGCGTCACTGCACAAGTTTGCTTACA	660
	L W A P T G G C C P G A S L H K F A Y N	
661	ATGACCAGGGCCAGGTGCGGCTTCGAGCCGGGCTGCCCATCTACGAGTGCAACTCCCCGT	720
	D Q G Q V R L R A G L P I Y E C N S R C	
721	GCCGCTGCGGCTATGACTGCCCAAATCGTGTGGTACAGAAGGGTATCCGATATGACCTCT	780
	R C G Y D C P N R V V Q K G I R Y D L C	
781	GCATCTTCCGGACGGATGATGGGCGTGGCTGGGGCGTCCGCACCCTGGAGAAGATTCCGA	840
	I F R T D D G R G W G V R T L E K I R K	
841	AGAACAGCTTCGTCATGGAGTACGTGGGAGAGATCATTACCTCAGAGGAGGCAGAGCGGC	900
	N S F V M E Y V G E I I T S E E A E R R	
901	GGGGCCAGATCTACGACCGTCAGGGCGCCACCTACCTCTTTGACCTGGACTACGTGGAGG	960
	G Q I Y D R Q G A T Y L F D L D Y V E D	
961	ACGTGTACACCGTGGATGCCGCTACTATGGCAACATCTCCCACTTTGTCAACCACAGTT	1020
	V Y T V D A A Y Y G N I S H F V N H S C	
1021	GTGACCCCAACCTGCAGGTGTACAACGTCTTCATAGACAACCTTGACGAGCGGCTGCCCC	1080
	D P N L Q V Y N V F I D N L D E R L P R	
1081	GCATCGCTTTCTTTGCCACAAGAACCATCCGGGCAGGCGAGGAGCTCACCTTTGATTACA	1140
	I A F F A T R T I R A G E E L T F D Y N	

Fig. 7/2

1141	ACATGCAAGTGGACCCCGTGGACATGGAGAGCACCCGCATGGACTCCAACCTTTGGCCTGG	1200
	M Q V D P V D M E S T R M D S N F G L A	
1201	CTGGGCTCCCTGGCTCCCCTAAGAAAGCGGGTCCGTATTGAATGCAAGTGTGGGACTGAGT	1260
	G L P G S P K K R V R I E C K C G T E S	
1261	CCTGCCGCAAATACCTCTTCTAGCCCTTAGAAGTCTGAGGCCAGACTGACTGAGGGGGCC	1320
	C R K Y L F *	
1321	TGAAGCTACATGCACCTCCCCACTGCTGCCCTCCTGTCGAGAATGACTGCCAGGGCCTC	1380
1381	GCCTGCCTCCACCTGCCCCACCTGCTCCTACCTGCTCTACGTCAGGGCTGTGGCCGTG	1440
1441	GTGAGGACCGACTCCAGGAGTCCCTTTCCCTGTCCAGCCCCATCTGTGGGTGCACTT	1500
1501	ACAAACCCCCACCCACCTTCAGAAATAGTTTTTCAACATCAAGACTCTCTGTGCGTTGGGA	1560
1561	TTCATGGCCTATTAAGGAGGTCCAAGGGGTGAGTCCCAACCCAGCCCCAGAATATATTTG	1620
1621	TTTTTGACCTGCTTCTGCCTGGAGATTGAGGGGTCTGCTGCAGGCCTCCTCCCTGCTGC	1680
1681	CCCAAAGGTATGGGGAAGCAACCCAGAGCAGGCAGACATCAGAGGCCAGAGTGCCTAGC	1740
1741	CCGACATGAAGCTGGTTCCCCAACACAGAACTTTGTACTAGTGAAGAAAGGGTCCC	1800
1801	TGGCCTACGGGCTGAGGCTGGTTTCTGCTCGTGCTTACAGTGCTGGGTAGTGTGGCCCT	1860
1861	AAGAGCTGTAGGGTCTCTTCTTCAGGGCTGCATATCTGAGAAGTGGATGCCACATGCCA	1920
1921	CTGGAAGGGAAGTGGGTGTCCATGGGCCACTGAGCAGTGAGAGGAAGGCAGTGCAAGCT	1980
1981	GGCCAGCCCTGGAGGTAGGCTGGGACCAAGCTCTGCCTTCACAGTGCAAGGTACCT	2040
2041	AGGGCTCTTGGGAGCTCTGCGGTTGCTAGGGGCCCTGACCTGGGGTGTATGACCGCTGA	2100
2101	CACCACTCAGAGCTGGAACCAAGATCTAGATAGTCCGTAGATAGCACTTAGGACAAGAAT	2160
2161	GTGCATTGATGGGGTGGTGATGAGGTGCCAGGCACTAGGTAGAGCACCTGGTCCACGTGG	2220
2221	ATTGTCTCAGGGAAGCCTTGAAAACACGGAGGTGGATGCCAGGAAAGGGCCCATGTGGC	2280
2281	AGAAGGCAAAGTACAGGCCAAGAATTGGGGGTGGGGGAGATGGCTTCCCCACTATGGGAT	2340
2341	GACGAGGCGAGAGGGAAGCCCTTGCTGCCTGCCATTCCCAGACCCAGCCCTTTGTGCTC	2400
2401	ACCCTGGTTCCACTGGTCTCAAAAGTCACCTGCCTACAAATGTACAAAAGCGAAGGTTT	2460
2461	TGATGGCTGCCTTGCTCCTTGCTCCCCACCCCTGTGAGGACTTCTCTAGGAAGTCCTT	2520
2521	CCTGACTACCTGTGCCCAGAGTGCCCCTACATGAGACTGTATGCCCTGCTATCAGATGCC	2580
2581	AGATCTATGTGTCTGTCTGTGTGCCATCCCGCGGGCCCCCAGACTAACCTCCAGGCAT	2640
2641	GGACTGAATCTGGTTCTCCTCTTGTACACCCCTCAACCCTATGCAGCCTGGAGTGGGCAT	2700
2701	CAATAAATGAACTGTCGACTGAAAAAAAAA	2732

① ②

B52

Fig. 9

A

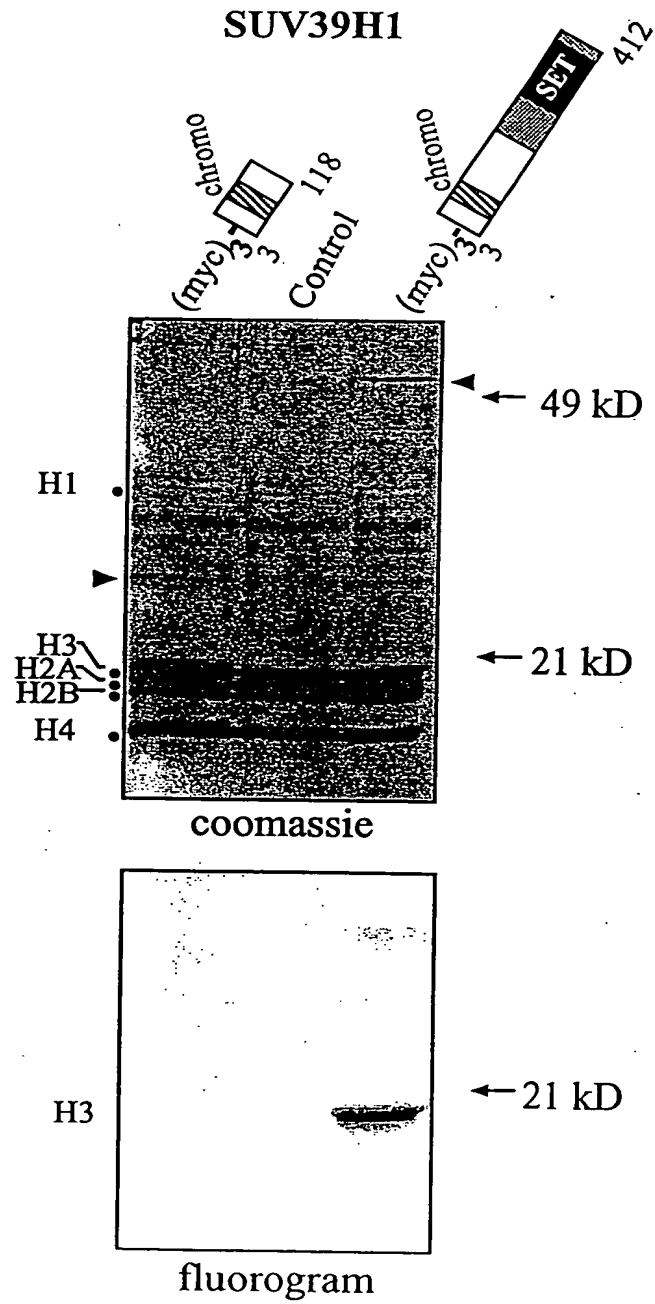


Fig. 9

B

Suv39h1

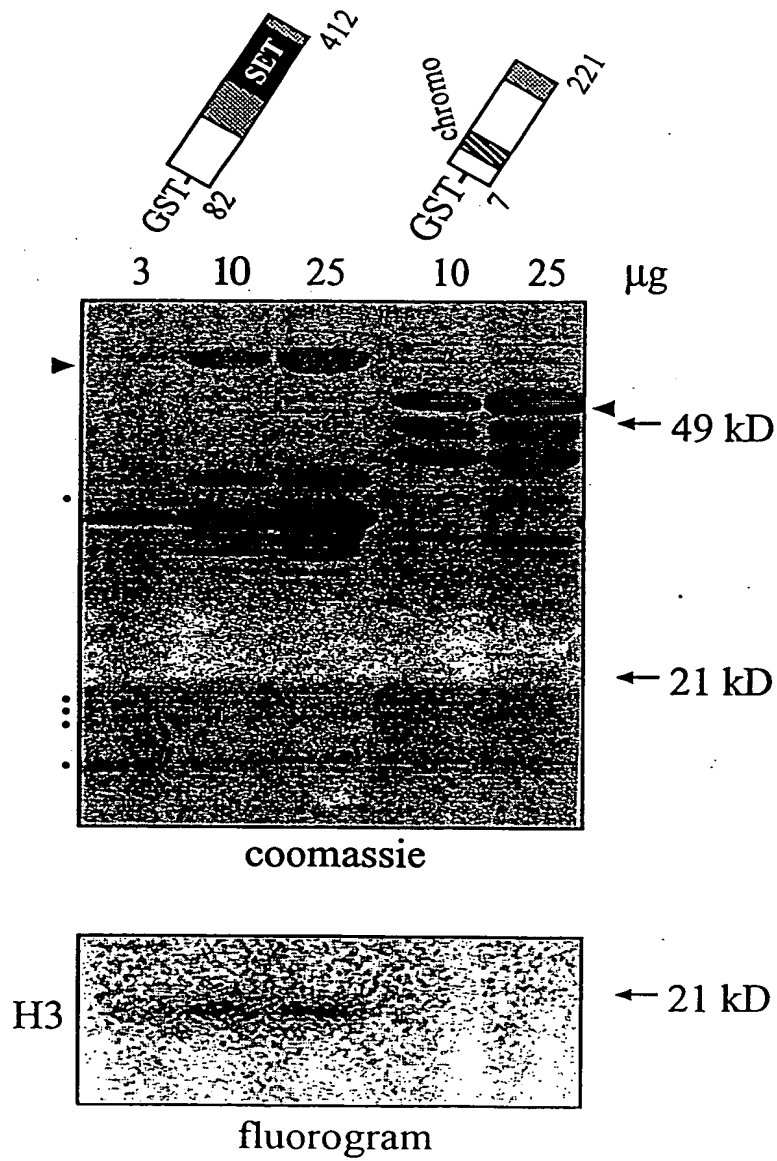


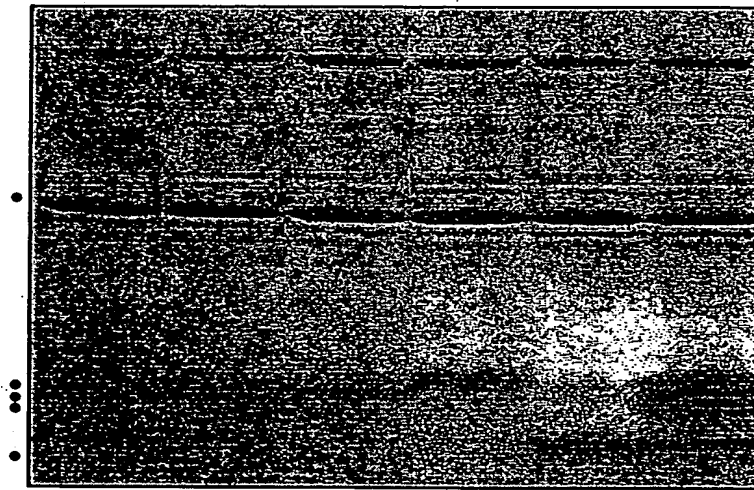
Fig. 10

A

Suv39h1

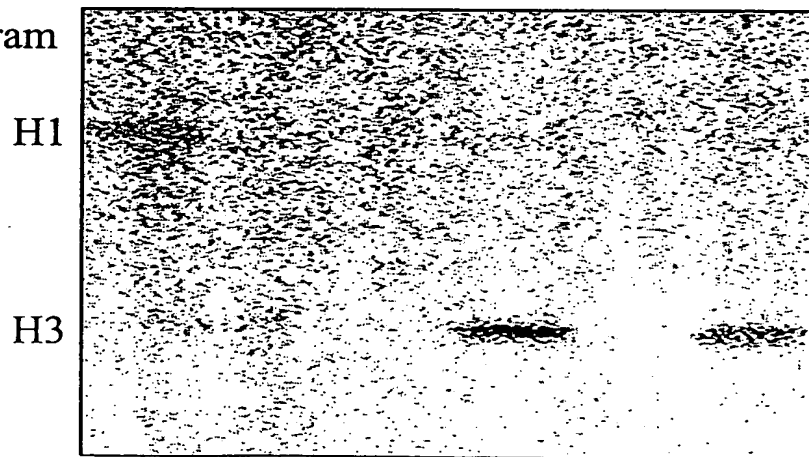


coomassie



H1 H2A H2B H3 H4 all

fluorogram



H1

H3

← 49 kD

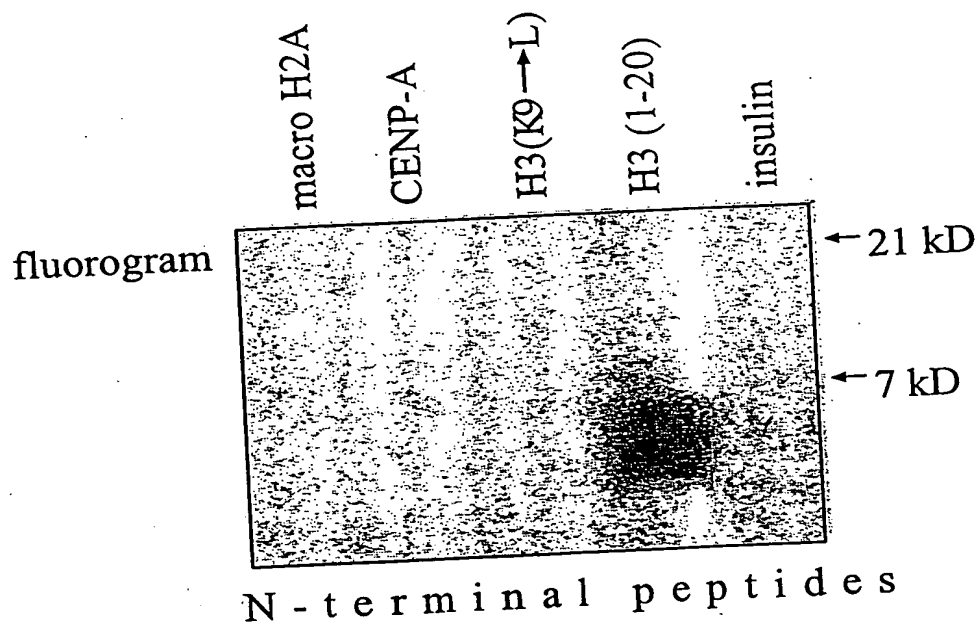
← 21 kD

← 49 kD

← 21 kD

Fig. 10

B



C

